1163-92-722 **Nicole Pagane**, **Devany West**, **Quinn MacPherson**, **Bruno Beltran**, **Andrew J Spakowitz** and **Viviana I Risca*** (vrisca@rockefeller.edu). *A Monte Carlo simulation framework for interpreting sub-kilobase chromatin folding data from RICC-seq.* Preliminary report.

The sub-kilobase structure of chromatin—the nucleosome-bound state of DNA found in the nuclei of eukaryotic cells—has undergone a recent re-evaluation in light of experiments showing it is more heterogeneous than previously thought. Chromatin structure at this length scale determines the local geometry and accessibility of binding sites on DNA for proteins driving critical processes like transcription. It has been difficult to probe in cells because it is densely packed and the weak interactions that shape it are easily perturbed. We have recently developed RICC-seq, a method for probing chromatin structure in a minimally perturbative way using ionizing radiation that generates population-averaged measurements. To generate chromatin structure ensembles for comparison with and interpretation of the pairwise DNA-DNA contact data RICC-seq provides, we describe a chromatin Monte Carlo simulation framework based on our previous code {wlcsim} that includes a stretchable-shearable worm-like chain approximation of DNA, explicit twist and steric constraints, and coarse-grained rigid body nucleosome representations based on crystal structures. We discuss how chromatin fiber geometry affects compaction and compare results with data from RICC-seq experiments in cultured cells. (Received September 11, 2020)